

Papahānaumokuākea Marine National Monument Permit Application Cover Sheet

This Permit Application Cover Sheet is intended to provide summary information and status to the public on permit applications for activities proposed to be conducted in the Papahānaumokuākea Marine National Monument. While a permit application has been received, it has not been fully reviewed nor approved by the Monument Management Board to date. The Monument permit process also ensures that all environmental reviews are conducted prior to the issuance of a Monument permit.

Summary Information

Applicant Name: Joshua Reece, M.S., Ph.D. Candidate

Affiliation: Washington University in Saint Louis

Permit Category: Research

Proposed Activity Dates: Three cruises between June 1, 2008 to September 20, 2008

Proposed Method of Entry (Vessel/Plane): Vessel

Proposed Locations: Nihoa, Ni'ihau, Necker, French Frigate Shoals, Gardner, Maro, Laysan, Lisianski, Pearl and Hermes, Midway, Kure

Estimated number of individuals (including Applicant) to be covered under this permit:
15

Estimated number of days in the Monument: Three cruises of approximately 25 days

Description of proposed activities: (complete these sentences):

a.) The proposed activity would...

The 2008 NWHI Lobster tagging cruise uses Fathoms-Plus (F-plus) box-like funnel traps to sample and tag lobster. Moray eels are frequently caught as bycatch. The proposed activity would allow for a small number of moray eel species to be preserved for studies of molecular genetics, morphology, and diet. In addition, the pier at Midway Island is a highly productive area for sampling moray eels and can be easily sampled from land at night when boat operations are not permitted. The proposed activity would allow for a representative sample of moray eel species to be taken by the use of lobster traps. In addition, other researchers collecting during two other cruises would be allowed to deploy traps for use in non-lethal sampling of their target species and collecting moray eels caught as by-catch.

b.) To accomplish this activity we would

The proposed activity would allow researchers already conducting sampling of other species and catching moray eels as bycatch to broaden the scientific impact of their sampling by removing a representative sample of moray eels for future analyses. This sampling is not time consuming, dangerous or costly, and will greatly enhance our understanding of moray eels, connectivity among the Northwest Hawaiian Islands, and the ecological role of moray eels as key predators.

Moreover, the sample sizes requested are highly unlikely to impact local or regional populations of moray eels or their ecological role on the coral reef. This claim is based on our preliminary data documenting high levels of gene flow and large effective population sizes (see background information below) in moray eels within the Papahānaumokuākea Marine National Monument.

c.) This activity would help the Monument by ...

This activity would help the monument in two ways. First, this work will identify population genetic structure in an abundant and ecologically important group of coral reef fishes. Population genetic structure describes the pattern of genetic diversity over a specified geographic area. Understanding how moray eel populations are connected or disjunct from one another informs management decisions that depend on estimates of gene flow and population size. Secondly, this research will elucidate species boundaries in moray eels. Our preliminary work is based on non-lethal sampling in which an organism was caught, keyed out to species, and then sampled for a rice grain sized piece of tissue and released. Non-lethal sampling is preferred when possible, however, our preliminary results identify extremely strange patterns. Repeatedly, individuals identified as the same species by morphology were not the same species genetically, and also individuals identified at different species by morphology were sometimes the same species genetically. This pattern is not limited to our work or to the Papahānaumokuākea Marine National Monument, and is repeated in museum collections for which voucher specimens are available, suggesting that the pattern is not due to misidentification but to a real pattern of phenotypic plasticity. Collection of voucher specimens from the Papahānaumokuākea Marine National Monument will allow for consistent species identification and detailed morphological and skeletal analyses to describe biologically realistic species. From the perspective of the monument, it is impossible to manage or protect species when the fundamental species unit is ambiguous or unknown. This small level of lethal sampling will have the long-lasting benefit of delimiting species boundaries for accurate management in the future.

Other information or background: The proposed sampling is largely based on a preliminary body of work generated by Joshua Reece at Washington University. His results are summarized through two figures in Appendix A. Figure 1 is a multilocus Bayesian phylogenetic reconstruction with an insert that depicts mitochondrial and nuclear phylogenetic reconstructions independently. This phylogeny demonstrates that species as defined by morphological characters do not form monophyletic groups, nor is there geographic clustering of species within the phylogeny. In other words, when we examine genetic patterns, we see that all organisms identified as one "species" do not form a single group that excludes all other "species." The congruency among loci in terms of phylogenetic placement rules out alternative explanations of hybridization or ancestral polymorphism, and leaves two alternatives: plasticity or misidentification. The only way to distinguish among these alternatives is by examining voucher specimens linked to DNA sequences to rule out misidentification and to specify which features currently used to identify species are uninformative. Figure 2 highlights and expands upon the lack of geographic clustering observed in Figure 1 by focusing on an example species, *Gymnothorax undulatus*. As the figure denotes, mitochondrial cytochrome b haplotypes are not clustered by geography, such that individuals sampled in Panama

are just as likely to be closely related genetically to individuals in South Africa as they are to other members of the same species in Panama. Moreover, three other species have genes that place them within the gene pool of *Gymnothorax undulatus*, but they clearly have morphologies that distinguish them as other species. The geographic expanse over which connectivity of mitochondrial haplotypes is maintained is incredible and spans over 20,000 kilometers. This suggests that moray eel larvae disperse great distances, which is not surprising given that moray eels have the longest pelagic larval durations among other coral reef fishes (Hourigan and Reese, 1987). Lastly, we have generated sufficient preliminary data to estimate effective population sizes based on standing genetic diversity. We have generated estimates of effective population sizes based on cytochrome b variation for reciprocally monophyletic clades for each of the following species sampled only from the Papahānaumokuākea Marine National Monument (estimated number of individuals in parentheses): *Gymnothorax undulatus* (2.75 million), *Gymnothorax eurostus* (3.14 million), *Gymnothorax steindachneri* (1.14 million), and *Gymnothorax flavimarginatus* (480,000). These estimates are exceedingly large and likely result from connectivity with reef systems outside of the Monument. In summary, given the high level of connectivity and large effective population sizes of moray eels in the Papahānaumokuākea Marine National Monument, lethal sampling is extremely unlikely to have any negative effects on demographic patterns on any time scale.